

### Amendments to the Specification

Please replace the paragraph beginning at page 2, line 17, with the following rewritten paragraph:

-- **Figures 2A-2B** ~~shows~~show a 1588 bp DNA sequence comprising the *Brassica napus* *FAE1* transcription regulatory sequence. --

Please replace the paragraph beginning at page 2, line 19, with the following rewritten paragraph:

-- **Figures 3A-3C** ~~shows~~show a 1069 bp DNA sequence comprising *Lunaria annua* *FAE1* transcription regulatory sequence. --

Please replace the paragraph beginning at page 2, line 21, with the following rewritten paragraph:

-- **Figures 4A-4C** ~~shows~~show an alignment of the *Arabidopsis thaliana* (*A. t.*), *Lunaria annua* (*L. a.*) and *Brassica napus* (*B. n.*) transcription regulatory sequences. Asterisks below the sequences indicate identical nucleotides in each of the three sequences. A number of putative cis-acting sequence motifs are identified in the *A. thaliana* sequence: an EM 1 ABA box at-44bp to-36bp having the sequence ACATCTCAT, for which the published consensus sequence is ACGTGTCAT (Rowley, D. L. and Herman. E. M. (1997), Biochimica et Biophysica Acta 1345: 1-4); an A-300 box at-51bp to-46bp having the sequence TGCAAT, for which the published consensus sequence is TG (T/A/C) AAA (G/T) (Morton et al. (1994) in Seed Development and Germination (Kigel, J. and Gallili, G., eds.) pp. 103-138 Marcel Dekker. New York); G-box 1 at-105 to-100 bp having the sequence CACATG, for which is the consensus sequence is CACCTG, and G-box 2 at-164 to-159 bp having the sequence CAACTT, for which the consensus sequence is CAACTG (Kawogoe, Y. and Murai, N. (1992) Plant J. 2: 927-936; CE1 element at-226 to-218 bp having the sequence TTCCATCGA. for which the consensus sequence is TGCCACCGG. and a CE3 element at 381bp to-369 bp having the sequence ACACATTCCCTC, for which the consensus sequence is ACGCGTGTCTC (Shen et al., (1996) Plant Cell 8: 1107-1119). Not highlighted is a putative RY repeat motif at-53bp to-47bp having the sequence CATGCAA, for

which the consensus sequence is CATGCAT (Dickinson et al. (1988) Nucleic Acid Res. 16: 371; Lelievre et al. (1992) Plant Physiol. 98: 387-391). Also shown, as Con. 4, is a consensus sequence, wherein R=G or A, Y=T/U or C, M=A or C, K=G or T/U, S=G or C, W=A or T/U, B=G or C or T/U, D=A or G or T/U, H=A or C or T/U, V=A or G or C and N=A or G or C or T/U. –

*Please replace the paragraph beginning at page 3, line 22, with the following rewritten paragraph:*

-- **Figures 7A-7B** ~~shows~~ show an alignment of the *Brassica napus* (B.n.) and *Lunaria annua* (L. a.) *FEA1* transcription regulatory sequences. Asterisks below the sequences indicate identical nucleotides in each of the two sequences. –

*Please replace the paragraph beginning at page 3, line 25, with the following rewritten paragraph:*

-- **Figures 8A-8B** ~~shows~~ show an alignment of the *Brassica napus* (B. n.) and *Arabidopsis thaliana* (A. t.) *FEA1* transcription regulatory sequences. Asterisks below the sequences indicate identical nucleotides in each of the two sequences.--

**Amendments to the Drawings**

The attached sheets of drawings includes changes to Figs. 1 through 8. These sheets replace the original sheets of drawings.

**Attachments:** Replacement sheets (15)  
Annotated sheets (15)